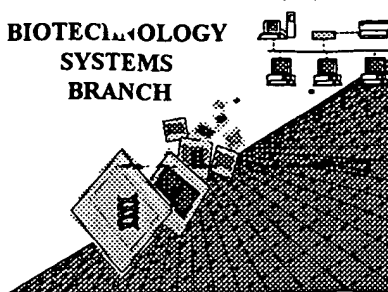


0270

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



**RAW SEQUENCE LISTING**  
**ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/679,687  
Source: OIPE  
Date Processed by STIC: 10/19/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/679,687

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                         <400> sequence id number  
                         000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                         In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                         Please explain source of genetic material in <220> to <223> section.  
                         (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
                         file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
                         Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING                      DATE: 10/19/2000  
PATENT APPLICATION:    US/09/679,687      TIME: 11:29:17

Input Set : A:\BB1162 US NA Seq Listing.txt  
Output Set: N:\CRF3\10192000\I679687.raw

3 <110> APPLICANT: Allen, Stephen M.  
4        Hitz, William D.  
5        Rafalski, J. Antoni  
7 <120> TITLE OF INVENTION: SUCROSE TRANSPORT PROTEINS  
9 <130> FILE REFERENCE: BB1162 US NA  
OK> 11 <140> CURRENT APPLICATION NUMBER: US/09/679,687  
12 <141> CURRENT FILING DATE: 2000-10-05  
14 <150> PRIOR APPLICATION NUMBER: ~~60/081,148~~  
W--> 15 <151> PRIOR FILING DATE: April 9, 1998 → 1998-04-09  
17 <150> PRIOR APPLICATION NUMBER: ~~PCT/US99/07562~~  
W--> 18 <151> PRIOR FILING DATE: April 7, 1999 → 1999-04-07  
OK 20 <160> NUMBER OF SEQ ID NOS: 28  
22 <170> SOFTWARE: Microsoft Office 97

Does Not Comply  
Corrected Diskette Needed

use this date format  
when employing new  
sequence header format

ERRORED SEQUENCES

see following pages for more errors

<210> 19  
 <211> 2083  
 <212> DNA  
 <213> Triticum aestivum

<400> 19

gcacgagcac	accacaccac	acctctctct	ctctcaactcg	cacttttcgc	tctcgtctcc	60
tcctcttcct	cctcccgtca	gacccttctt	ccccggcggt	gatccgatca	acgtcctcct	120
cgtcctgcc	cctagatcct	tggccgggca	gggatacgcc	gtagaattga	taggcgaacg	180
gacgaggtgg	tgatcgccag	ggcggcctct	ctgccatggc	gcgcggcgga	ggcaacggcg	240
aggtggagct	ctcggtcggg	gtcggcgggc	gaggcgggcg	cgccgcgggc	gggggggagc	300
aaccgcgct	ggacatcagc	ctcggcagac	tcctcctcgc	cggcatggtc	gccggcgggc	360
tgcagtacgg	atgggcgctc	cagctctccc	tgctcacccc	ctacgtccag	actctgggac	420
tttcgcatgc	tctgacttca	ttcatgtggc	tctgcggccc	tattgctgga	ttagtggttc	480
aaccatgcgt	tgggtctctac	agtgacaagt	gcacatctag	atggggaaga	cgcagaccgt	540
ttattctgac	aggatgcata	ctcatctgca	ttgctgttgt	ggtcgtcggc	ttctcggctg	600
acattggagc	tgggtctgggt	gacagcaagg	aagagtgcag	tctctatcat	gggcctcggt	660
ggcacgctgc	aatttgttat	gttcttggtat	tctggctcct	tgacttctcc	aacaacactg	720
tgcaagggtcc	agcgcgtgct	ctgatggctg	atttatcagc	tcagcatgga	cccagtgcag	780
caaattcaat	cttctgttct	tggatggcgc	taggaaatat	ccttggtata	tcctctgggt	840
ccacaaacaa	ctggcacaag	tgggttccgt	tcctccggac	aagggttgc	tgtgaagcct	900
gcgcaaactct	gaaaggcgca	tttctgggtg	cagtgtgtgt	cctggccttc	tgtttggtga	960
taactgtgat	cttcgccaag	gagataccgt	acaaggcgat	tgcgcccctc	ccaacaaagg	1020
gcaatggcca	gggtgaagtc	gagcccacog	ggcogctcgc	cgtgttcaaa	ggcttcaaga	1080
acttgccctcc	tgnaatgccc	tgggtgctcc	tcgtcaactgg	cctcacctgg	ctgtcctggt	1140
tccccctcat	cctgtacgac	accgactgga	tgggtcgtga	gatctaccac	ggtgacccca	1200
agggaacccc	cgacgaggcc	aacgcgttcc	aggcaggtgt	cagggccggg	gcgttcggcc	1260
tgctactcaa	ctcggtcgtc	ctgggggttc	gctcgttctc	gatcgagccg	ctgtgcaaga	1320
ggctaggccc	gcgggtggtg	tgggtgtcga	gcaacttctc	cgtctgcctc	tccatggccg	1380
cgatttgcat	cataagctgg	tgggtacttc	aggacttgca	tgggtatata	cagcacgcca	1440
tcaccgccag	caaggagatc	aagatcgtct	ccctcgcctc	cttcgccttc	ctcggaatcc	1500
ctctcgccat	tctgtacagt	gtccctttcg	cggtgacggc	gcagctggcg	gcgaagagag	1560
gcgggtggcca	agggctgtgc	acgggcgtgc	tcaacatogc	catcgtgata	cccagggtga	1620
tcacgcgggt	gggggcgggg	ccgtgggacg	agctgttcgg	caagggaac	atcccggcgt	1680
tggcatggc	ctccgccttc	gcgctcatcg	gcggcatcgt	cggcatattc	ctgctgcca	1740
agatctccag	gcgccagttc	cgggcggtca	gcggcgggcg	tactgagca	tggccaaggc	1800
cggagggtccc	agcccagccc	gccatttacc	aaattttcgc	ataggcgtaa	ctagggtggct	1860
ctcgccctaa	gactccgtag	agcagaataa	gaattgtgag	gaacctgtat	gtgttggtgc	1920
tgtatgtgcg	tgtaagtcag	tgctgttagc	ggaaaatgga	cagaggaatg	tgggcatcca	1980
tcaccggctg	gggtgtcgtc	tttgggttgt	gacttgtgtg	tagcaaacca	aggtgatcaa	2040
gtgaggggaa	atgaatggat	gatgaacttt	cagcgacaaa	aaa		2083

→ see  
 item 10  
 on Enon  
 Summary  
 Sheet

09/679,687 3

<210> 25 *insert hard return*  
<211> 501  
<212> PRT *insert hard return*  
<213> Daucus carota<400> 25Met Ala Gly Pro Glu Ala Asp Arg Asn Arg His Arg  
Gly Gly Ala Thr 1 5 10 15  
*insert hard return*  
Ala Ala Pro Pro Pro Arg Ser Arg Val Ser Leu Arg Leu Leu Leu Arg  
20 25 30

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/679,687

DATE: 10/19/2000

TIME: 11:29:18

Input Set : A:\BB1162 US NA Seq Listing.txt

Output Set: N:\CRF3\10192000\I679687.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number  
 L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
 L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
 L:826 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13  
 L:826 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13  
 L:900 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14  
 L:900 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14  
 L:903 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14  
 M:340 Repeated in SeqNo=14  
 L:1062 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19  
 L:1062 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19  
 L:1062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19  
 L:1062 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19  
 L:1062 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19  
 L:1587 M:280 W: Numeric Identifier already exists, Length not replaced.  
 L:1588 M:280 W: Numeric Identifier already exists, Type not replaced.  
 L:1589 M:280 W: Numeric Identifier already exists, Organism not replaced.  
 L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (28) Counted (27)